

1 GAATATGATG ACCCTAATGC AACAAATATCT AACATACTAT CCGAGCTTCG
51 GTCATTTGGA AGAACTGCAG ATTTTCCTCC TTCAAATAA AAGTCAGGTT
101 ATGGAGAACA TGTATGCTAT GTTCTTGATT GCTTCGCTGA AGAAGCATTG
151 AAATATATTG GTTTCACCTG GAAAAGGCCA ATATACCCAG TAGAAGAATT
201 AGAAGAAGAA AGCGTTGCAG AAGATGATGC AGAATTAACA TTAAATAAAG
251 TGGATGAAGA ATTTGTGGAA GAAGAGACAG ATAATGAAGA AAACCTTTATT
301 GATCTCAACG TTTTAAAGGC CCAGACATAT CACTTGGATA TGAACGAGAC
351 TGCCAAACAA GAAGATATTT TGGAATCCAC AACAGATGCT GCAGAAATGGA
401 GCCTAGAAGT GGAACGTGTA CTACCGCAAC TGAAAGTCAC GATTAGGACT
451 GACAATAAGG ATTGGAGAAT CCATGTTGAC CAAATGCACC AGCACAGAAG
501 TGGAATTGAA TCTGCTCTAA AGGAGACCAA GGGATTTTGT GACAAACTCC
551 ATAATGAAAT TACTAGGACT TTGGAAAAGA TCAGCAGCCG AGAAAAGTAC
601 ATCAACAATC AGCCGGGAGC CCATGGAGCA CTGTCCTCAG AGATGCGCAG
651 GTTAGGCTCA CTGTCTAGGC CAGGCCACC TTAGTCACTG TGGACTGGCA
701 ATGGAAGCTC TTCCTGGACA CACCTGCCCT AGCCCTCACC CTGGGGTGGG
751 AGAGAAATGA GCTTGGCTTG CAACTCAGAC CATTCCACGG AGGCATCCTC
801 CCCTTCCCTG GGCTGGTGAA TAAAAGTTTC CTGAGGTCAA GGAATTCCTT
851 TTCCCTGCCA AAATGGTGTC CAGAACTTTG AGGCCAGAGG TGATCCAGTG

FIGURE 1A

901 ATTTGGGAGC TGCAGGTCAC ACAGGCTGCT CAGAGGGCTG CTGAACAGGA
951 TGTCTCTCGGA CGACAGGCAC CTGGGCTCCA GCTGCGGCTC CTTTCATCAAG
1001 ACTGAGCCGT CCAGCCCGTC CTCGGGCATA GATGCCCTCA GCCACCACAG
1051 CCCAGTGGC TCGTCCGACG CCAGCGGCGG CTTTGGCCTG GCCCTGGGCA
1101 CCCACGCCAA CGGTCTGGAC TCGCCACCCA TGTTTGCAGG CGCCGGGCTG
1151 GGAGGCACCC CATGCCGCAA GAGCTACGAG GACTGTGCCA GCGGCATCAT
1201 GGAGGACTCG GCCATCAAGT GCGAGTACAT GCTCAACGCC ATCCCCAAGC
1251 GCCTGTGCCT CGTGTGCGGG GACATTGCCT CTGGCTACCA CTACGGCGTG
1301 GCCTCCTGCG AGGCTTGCAA GGCCTTCTTC AAGAGGACTA TCCAAGGGAA
1351 CATTGAGTAC AGCTGCCCGG CCACCAACGA GTGCGAGATC ACCAAACGGA
1401 GGCACAAGTC CTGCCAGGCC TGCCGCTTCA TGAAATGCCT CAAAGTGGGG
1451 ATGCTGAAGG AAGGTGTGCG CCTTGATCGA GTGCGTGGAG GCCGTCAGAA
1501 ATACAAGCGA CGGCTGGACT CAGAGAGCAG CCCATACCTG AGCTTACAAA
1551 TTTCTCCACC TGCTAAAAAG CCATTGACCA AGATTGTCTC ATACCTACTG
1601 GTGGCTGAGC CGGACAAGCT CTATGCCATG CCTCCCCCTG GTATGCCTGA
1651 GGGGGACATC AAGGCCCTGA CCACTCTCTG TGACCTGGCA GACCGAGAGC
1701 TTGTGGTCAT CATTGGCTGG GCCAAGCACA TCCCAGGCTT CTCAAGCCTC
1751 TCCCTGGGGG ACCAGATGAG CCGCTGCGAG AGTGCCTGGA TGGAAATCCT

FIGURE 1B

1801 CATCCTGGGC ATCGTGTACC GCTCGCTGCC CTACGACGAC AAGCTGGTGT
1851 ACGCTGAGGA CTACATCATG GATGAGGAGC ACTCCCGCCT CGCGGGGCTG
1901 CTGGAGCTCT ACCGGGCCAT CCTGCAGCTG GTACGCAGGT ACAAGAAGCT
1951 CAAGGTGGAG AAGGAGGAGT TTGTGACGCT CAAGGCCCTG GCCCTCGCCA
2001 ACTCCGATTC CATGTACATC GAGGATCTAG AGGCTGTCCA GAAGCTGCAG
2051 GACCTGCTGC ACGAGGCACT GCAGGACTAC GAGCTGAGCC AGCGCCATGA
2101 GGAGCCCTGG AGGACGGGCA AGCTGCTGCT GACACTGCCG CTGCTGCGGC
2151 AGACGGCCGC CAAGGCCGTG CAGCACTTCT ATAGCGTCAA ACTGCAGGGC
2201 AAAGTGCCCA TGCACAACT CTCCTGGAG ATGCTGGAGG CCAAGGCCTG
2251 GGCCAGGGCT GACTCCCTTC AGGAGTGGAG GCCACTGGAG CAAGTGCCCT
2301 CTCCCCTCCA CCGAGCCACC AAGAGGCAGC ATGTGCATTT CCTAACTCCC
2351 TTGCCCCCTC CCCCATCTGT GGCCTGGGTG GGCAGTCTC AGGCTGGATA
2401 CCACCTGGAG GTTTTCCTTC CGCAGAGGGC AGGTGGCCA AGAGCAGCTT
2451 AGAGGATCTC CCAAGGATGA AAGAATGTCA AGCCATGATG GAAAATGCCC
2501 CTTCCAATCA GCTGCCTTCA CAAGCAGGGA TCAGAGCAAC TCCCCGGGGA
2551 TCCCCAATCC ACGCCCTTCT AGTCCAACCC CCCTCAATGA GAGAGGCAGG
2601 CAGATCTCAC CCAGCACTAG GACACCAGGA GGCCAGGGAA AGCATCTCTG
2651 GCTCACCATG TAACATCTGG CTTGGAGCAA GTGGGTGTTT TGCACACCAG
2701 GCAGCTGCAC CTCACTGGAT CTAGTGTTGC TGCAGGTGAC CTCACTTCAG
2751 AGCCCCCTCTA GCAGAGTGGG GCGGAAGTCC TGATGGTTGG TGTCCATGAG
2801 GTGGAAG (SEQ ID NO:1)

FIGURE 1C

1 GAATATGATGACCCTAATGCAACAATATCTAACATACTATCCGAGCTTCGGTCATTTGGA 60
 -----+-----+-----+-----+-----+-----+
 CTTATACTACTGGGATTACGTTGTTATAGATTGTATGATAGGCTCGAAGCCAGTAAACCT
 61 AGAACTGCAGATTTTCCTCCTTCAAAATTAAAGTCAGGTTATGGAGAACATGTATGCTAT 120
 -----+-----+-----+-----+-----+-----+
 TCTTGACGTCTAAAAGGAGGAAGTTTAAATTCAGTCCAATACCTCTTGACATACGATA
 121 GTTCTTGATTGCTTCGCTGAAGAAGCATTGAAATATATTGGTTTCACCTGGAAAAGGCCA 180
 -----+-----+-----+-----+-----+-----+
 CAAGAACTAACGAAGCGACTTCTTCGTAACCTTTATATAACCAAAGTGGACCTTTTCCGGT
 181 ATATACCCAGTAGAAGAATTAGAAGAAGAAAGCGTTGCAGAAGATGATGCAGAATTAACA 240
 -----+-----+-----+-----+-----+-----+
 TATATGGGTCATCTTCTTAATCTTCTTCTTCGCAACGTCTTCTACTACGTCTTAATTGT
 241 TTAAATAAAGTGGATGAAGAATTTGTGGAAGAAGAGACAGATAATGAAGAAAACCTTTATT 300
 -----+-----+-----+-----+-----+-----+
 AATTTATTTACCTACTTCTTAACACCTTCTTCTGTCTATTACTTCTTTTGAATAA
 301 GATCTCAACGTTTTAAAGGCCCGACATATCACTTGGATATGAACGAGACTGCCAAACAA 360
 -----+-----+-----+-----+-----+-----+
 CTAGAGTTGCAAAATTTCCGGGTCTGTATAGTGAACCTATACTTGCTCTGACGGTTTGT
 361 GAAGATATTTTGAATCCACAACAGATGCTGCAGAATGGAGCCTAGAAGTGGAACGTGTA 420
 -----+-----+-----+-----+-----+-----+
 CTTCTATAAAACCTTAGGTGTTGTCTACGACGTCTTACCTCGGATCTTCACCTTGCACAT
 421 CTACCGCAACTGAAAGTCACGATTAGGACTGACAATAAGGATTGGAGAATCCATGTTGAC 480
 -----+-----+-----+-----+-----+-----+
 GATGGCGTTGACTTTCAGTGCTAATCCTGACTGTTATTCCTAACCTCTTAGGTACAACCTG
 481 CAAATGCACCAGCACAGAAGTGAATTGAATCTGCTCTAAAGGAGACCAAGGGATTTTGT 540
 -----+-----+-----+-----+-----+-----+
 GTTTACGTGGTCTGTCTTCACCTTAACTTAGACGAGATTTCCTCTGGTTCCCTAAAAAC

FIGURE 2A

541 GACAAACTCCATAATGAAATTACTAGGACTTTGGAAAAGATCAGCAGCCGAGAAAAGTAC 600
 -----+-----+-----+-----+-----+-----+
 CTGTTTGAGGTATTACTTTAATGATCCTGAAACCTTTTCTAGTCGTCGGCTCTTTTCATG

 601 ATCAACAATCAGCCGGGAGCCCATGGAGCACTGTCCTCAGAGATGCGCAGGTTAGGCTCA 660
 -----+-----+-----+-----+-----+-----+
 TAGTTGTTAGTCGGCCCTCGGGTACCTCGTGACAGGAGTCTCTACGCGTCCAATCCGAGT

 661 CTGTCTAGGCCAGGCCACCTTAGTCACTGTGGACTGGCAATGGAAGCTCTTCCTGGACA 720
 -----+-----+-----+-----+-----+-----+
 GACAGATCCGSTCCGGGTGGAATCAGTGACACCTGACCGTTACCTTCGAGAAGGACCTGT

 721 CACCTGCCCTAGCCCTCACCTGGGGTGAAGAGAAATGAGCTTGGCTTGCAACTCAGAC 780
 -----+-----+-----+-----+-----+-----+
 GTGGACGGGATCGGGAGTGGGACCCACCTTCTCTTTACTCGAACCGAACGTTGAGTCTG

 781 CATTCACGGAGGCATCCTCCCCTTCCCTGGGGCTGGTGAATAAAAGTTTCTTGAGGTCAA 840
 -----+-----+-----+-----+-----+-----+
 GTAAGGTGCCTCCGTAGGAGGGGAAGGGACCCGACCACTTATTTCAAAGGACTCCAGTT

 841 GGACTTCCTTTTCCCTGCCAAAATGGTGTCCAGAACTTTGAGGCCAGAGGTGATCCAGTG 900
 -----+-----+-----+-----+-----+-----+
 CCTGAAGGAAAAGGGACGGTTTTACCACAGGTCTTGAAACTCCGGTCTCCACTAGGTCAC

 901 ATTTGGGAGCTGCAGGTACACAGGCTGCTCAGAGGGCTGCTGAACAGGATGTCTCTCGGA 960
 -----+-----+-----+-----+-----+-----+
 TAAACCCTCGACGTCCAGTGTGTCCGACGAGTCTCCCGACGACTTGTCCTACAGGAGCCT
 M S S D

 961 CGACAGGCACCTGGGCTCCAGCTGCGGCTCCTTCATCAAGACTGAGCCGTCCAGCCCGTC 1020
 -----+-----+-----+-----+-----+-----+
 GCTGTCCGTGGACCCGAGGTCGACGCCGAGGAAGTAGTTCTGACTCGGCAGGTCGGGCAG
 D R H L G S S C G S F I K T E P S S P S

FIGURE 2B

1021 CTCGGGCATAGATGCCCTCAGCCACCACAGCCCCAGTGGCTCGTCCGACGCCAGCGGCGG 1080
 -----+-----+-----+-----+-----+-----+
 GAGCCCGTATCTACGGGAGTCGGTGGTGTCTCGGGGTACCGAGCAGGCTGCGGTGCGCGCC
 S G I D A L S H H S P S G S S D A S G G

 1081 CTTTGGCCTGGCCCTGGGCACCCACGCCAACGGTCTGGACTCGCCACCCATGTTTGCAGG 1140
 -----+-----+-----+-----+-----+-----+
 GAAACCGGACCGGGACCCGTGGGTGCGGTTGCCAGACCTGAGCGGTGGGTACAAACGTCC
 F G L A L G T H A N G L D S P P M F A G

 1141 CGCCGGGCTGGGAGGCACCCCATGCCGCAAGAGCTACGAGGACTGTGCCAGCGGCATCAT 1200
 -----+-----+-----+-----+-----+-----+
 GCGGCGCGACCCCTCCGTGGGGTACGGCGTTCTCGATGCTCCTGACACGGTCGCGGTAGTA
 A G L G G T P C R K S Y E D C A S G I M

 1201 GGAGGACTCGGCCATCAAGTGCGAGTACATGCTCAACGCCATCCCCAAGCGCCTGTGCCT 1260
 -----+-----+-----+-----+-----+-----+
 CCTCCTGAGCCGCTAGTTTACGCTCATGTACGAGTTGCGGTAGGGGTTGCGGACACGGA
 E D S A I K C E Y M L N A I P K R L C L

 1261 CGTGTGCGGGGACATTGCCTCTGGCTACCACTACGGCGTGGCCTCCTGCGAGGCTTGCAA 1320
 -----+-----+-----+-----+-----+-----+
 GCACACGCCCCCTGTAACGGAGACCGATGGTGTATGCCGCACCGGAGGACGCTCCGAACGTT
V C G D I A S G Y H Y G V A S C E A C K

 1321 GGCCTTCTTCAAGAGGACTATCCAAGGGAACATTGAGTACAGCTGCCCCGGCCACCAACGA 1380
 -----+-----+-----+-----+-----+-----+
 CCGGAAGAAGTTCTCCTGATAGGTTCCCTTGTAACATCATGTCGACGGGCCGGTGGTTGCT
A F F K R T I Q G N I E Y S C P A T N E

 1381 GTGCGAGATCACCAACGGAGGCGCAAGTCCTGCCAGGCCTGCCGCTTCATGAAATGCCT 1440
 -----+-----+-----+-----+-----+-----+
 CACGCTCTAGTGGTTTGCCTCCGCGTTTACGACGGTCCGGACGGCGAAGTACTTTACGGA
C E I T K R R R K S C Q A C R F M K C L

FIGURE 2C

1441 CAAAGTGGGGATGCTGAAGGAAGGTGTGCGCCTTGATCGAGTGCGTGGAGGCCGTCAGAA 1500
 -----+-----+-----+-----+-----+-----+
 GTTTCACCCCTACGACTTCCTTCCACACGCGGAAGTAGCTCACGCACCTCCGGCAGTCTT
K V G M L K E G V R L D R V R G G R Q K

1501 ATACAAGCGACGGCTGGACTCAGAGAGCAGCCCATACCTGAGCTTACAAATTTCTCCACC 1560
 -----+-----+-----+-----+-----+-----+
 TATGTTTCGCTGCCGACCTGAGTCTCTCGTCGGGTATGGACTCGAATGTTTAAAGAGGTGG
 Y K R R L D S E S S P Y L S L Q I S P P

1561 TGCTAAAAAGCCATTGACCAAGATTGTCTCATACCTACTGGTGGCTGAGCCGGACAAGCT 1620
 -----+-----+-----+-----+-----+-----+
 ACGATTTTTTCGGTAACTGGTTCTAACAGAGTATGGATGACCACCGACTCGGCCTGTTTGA
 A K K P L T K I V S Y L L V A E P D K L

1621 CTATGCCATGCCTCCCCCTGGTATGCCTGAGGGGGACATCAAGGCCCTGACCACTCTCTG 1680
 -----+-----+-----+-----+-----+-----+
 GATACGGTACGGAGGGGGACCATACGGACTCCCCCTGTAGTTCCGGGACTGGTGAGAGAC
 Y A M P P P G M P E G D I K A L T T L C

1681 TGACCTGGCAGACCGAGAGCTTGTGGTCATCATTGGCTGGGCCAAGCACATCCCAGGCTT 1740
 -----+-----+-----+-----+-----+-----+
 ACTGGACCGTCTGGCTCTCGAACACCAGTAGTAACCGACCCGGTTCGTGTAGGGTCCGAA
 D L A D R E L V V I I G W A K H I P G F

1741 CTCAAGCCTCTCCCTGGGGGACCAGATGAGCCTGCTGCAGAGTGCCCTGGATGGAAATCCT 1800
 -----+-----+-----+-----+-----+-----+
 GAGTTCGGAGAGGGACCCCCTGGTCTACTCGGACGACGTCTCACGGACCTACCTTTAGGA
 S S L S L G D Q M S L L Q S A W M E I L

1801 CATCCTGGGCATCGTGTACCGCTCGCTGCCCTACGACGACAAGCTGGTGTACGCTGAGGA 1860
 -----+-----+-----+-----+-----+-----+
 GTAGGACCCGTAGCACATGGCGAGCGACGGATGCTGCTGTTTCGACCACATGCGACTCCT
 I L G I V Y R S L P Y D D K L V Y A E D

FIGURE 2D

1861 CTACATCATGGATGAGGAGCACTCCCGCCTCGCGGGGCTGCTGGAGCTCTACCGGGCCAT 1920
 -----+-----+-----+-----+-----+-----+
 GATGTAGTACCTACTCCTCGTGAGGGCGGAGCGCCCCGACGACCTCGAGATGGCCCGGTA
 Y I M D E E H S R L A G L L E L Y R A I

1921 CCTGCAGCTGGTACGCAGGTACAAGAAGCTCAAGGTGGAGAAGGAGGAGTTTGTGACGCT 1980
 -----+-----+-----+-----+-----+-----+
 GGACGTCGACCATGCGTCCATGTTCTTCGAGTTCCACCTCTTCCTCCTCAAACACTGCGA
 L Q L V R R Y K K L K V E K E E F V T L

1981 CAAGGCCCTGGCCCTCGCCAACTCCGATTCCATGTACATCGAGGATCTAGAGGCTGTCCA 2040
 -----+-----+-----+-----+-----+-----+
 GTTCCGGGACCGGGAGCGGTTGAGGCTAAGGTACATGTAGCTCCTAGATCTCCGACAGGT
 K A L A L A N S D S M Y I E D L E A V Q

2041 GAAGCTGCAGGACCTGCTGCACGAGGCACTGCAGGACTACGAGCTGAGCCAGCGCCATGA 2100
 -----+-----+-----+-----+-----+-----+
 CTTGACGTCCTGGACGACGTGCTCCGTGACGTCTGATGCTCGACTCGGTGCGGTACT
 K L Q D L L H E A L Q D Y E L S Q R H E

2101 GGAGCCCTGGAGGACGGGCAAGCTGCTGCTGACACTGCCGCTGCTGCGGCAGACGGCCGC 2160
 -----+-----+-----+-----+-----+-----+
 CCTCGGGACCTCCTGCCCCGTTTCGACGACGACTGTGACGGCGACGACGCCGTCTGCCGGCG
 E P W R T G K L L L T L P L L R Q T A A

2161 CAAGGCCGTGCAGCACTTCTATAGCGTCAAAGTGCAGGGCAAAGTGCCCATGCACAACT 2220
 -----+-----+-----+-----+-----+-----+
 GTTCCGGCACGTCGTGAAGATATCGCAGTTTGACGTCCCGTTTCACGGGTACGTGTTGA
 K A V Q H F Y S V K L Q G K V P M H K L

2221 CTTCTGGAGATGCTGGAGGCCAAGGCCTGGGCCAGGGCTGACTCCCTTCAGGAGTGGAG 2280
 -----+-----+-----+-----+-----+-----+
 GAAGGACCTCTACGACCTCCGGTTCCGGACCCGGTCCCGACTGAGGGAAGTCTCACCTC
 F L E M L E A K A W A R A D S L Q E W R

FIGURE 2E

9/23

19999Y

2281 GCCACTGGAGCAAGTGCCTCTCCCTCCACCGAGCCACCAAGAGGCAGCATGTGCATTT
 -----+-----+-----+-----+-----+-----+ 2340
 CGGTGACCTCGTTCACGGGAGAGGGGAGGTGGCTCGGTGGTTCTCCGTCGTACACGTAAA
 P L E Q V P S P L H R A T K R Q H V H F

2341 CCTAACTCCCTTGCCCCCTCCCCATCTGTGGCCTGGGTGGGCACTGCTCAGGCTGGATA
 -----+-----+-----+-----+-----+-----+ 2400
 GGATTGAGGGAACGGGGGAGGGGTAGACACCGGACCCACCCGTGACGAGTCCGACCTAT
 L T P L P P P P S V A W V G T A Q A G Y

2401 CCACCTGGAGGTTTTCTTCCGAGAGGGCAGGTTGGCCAAGAGCAGCTTAGAGGATCTC
 -----+-----+-----+-----+-----+-----+ 2460
 GGTGGACCTCCAAAAGGAAGGCGTCTCCCGTCCAACCGTTCTCGTCGAATCTCCTAGAG
 H L E V F L P Q R A G W P R A A * (SEQ ID NO:2)

2461 CCAAGGATGAAAGAATGTCAAGCCATGATGAAAATGCCCTTCCAATCAGCTGCCTTCA
 -----+-----+-----+-----+-----+-----+ 2520
 GGTTCCTACTTTCTTACAGTTCGGTACTACCTTTTACGGGGAAGGTTAGTCGACGGAAGT

2521 CAAGCAGGGATCAGAGCAACTCCCCGGGGATCCCCAATCCACGCCCTTCTAGTCCAACCC
 -----+-----+-----+-----+-----+-----+ 2580
 GTTCGTCCCTAGTCTCGTTGAGGGGCCCTAGGGGTAGGTGCGGGAAGATCAGGTTGGG

2581 CCCTCAATGAGAGAGGCAGGCAGATCTCAGCCAGCACTAGGACACCAGGAGGCCAGGGAA
 -----+-----+-----+-----+-----+-----+ 2640
 GGGAGTTACTCTCTCCGTCCGTCTAGAGTGGGTGCTGATCCTGTGGTCCTCCGGTCCCTT

2641 AGCATCTCTGGCTCACCATGTAACATCTGGCTTGGAGCAAGTGGGTGTTCTGCACACCAG
 -----+-----+-----+-----+-----+-----+ 2700
 TCGTAGAGACCGAGTGGTACATTGTAGACCGAACCTCGTTCACCCACAAGACGTGTGGTC

2701 GCAGCTGCACCTCACTGGATCTAGTGTGCTGCGAGTGACCTCACTTCAGAGCCCCCTCTA
 -----+-----+-----+-----+-----+-----+ 2760
 CGTCGACGTGGAGTGACCTAGATCACAACGACGCTCACTGGAGTGAAGTCTCGGGGAGAT

2761 GCAGAGTGGGGCGGAAGTCCTGATGGTTGGTGTCCATGAGGTGGAAG (SEQ ID NO:1)
 -----+-----+-----+-----+-----+-----+ 2807
 CGTCTACCCCGCCTTCAGGACTACCAACCACAGGTACTCCACCTTC (SEQ ID NO:29)

FIGURE 2F

10/23

19999 Y

MSSDDRHLGS SCGSFIKTEP SSPSSGIDAL SHHSPSGSSD ASGGFGLALG
THANGLDSPP MFAGAGLGGT PCRKSYEDCA SGIMEDSAIK CEYMLNAIPK
RLCLVCGDIA SGYHYGVASC EACKAFFKRT IQGNIEYSCP ATNECEITKR
RRKSCQACRF MKCLKVGM LK EGVRLDRVRG GRQKYKRRLD SESSPYLSLQ
ISPPAKKPLT KIVSYLLVAE PDKLYAMPPP GMPEGDIKAL TTLCDLADRE
LVVIIGWAKH IPGFSSLSLG DQMSLLQSAW MEILILGIVY RSLPYDDKLV
YAEDYIMDEE HSRLAGLLEL YRAILQLVRR YKKLKVEKEE FVTLKALALA
NSDSMYIEDL EAVQKLQDLL HEALQDYELS QRHEEPWRTG KLLLTPLLR
QTAAKAVQHF YSVKLQGVKVP MHKLFLEMLE AKAWARADSL QEWRPLEQVP
SPLHRATKRQ HVHFLTPLPP PPSVAWVGTA QAGYHLEVFL PORAGWPRAA
(SEQ ID NO:2)

FIGURE 3

1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA GAACATTTGT
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTTAT AGCTGGGGTG
101 CACAAATAAT GGTGCGCGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CCTTCTGCTC CTATCCTGGG
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGACTGCTCC AGCACCATTG
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCCAAG
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAAGTGGG
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTCGGCAGA
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG
901 ACAGTGACAT CAAAGCCCTC ACTACACTGT GTGACTTGGC CGACCGAGAG
951 TTGGTGGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAATTT
1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGAAGTTGTC

FIGURE 4A

1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAGAAA TACAAGAGCA
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTT AGAAGCTTCA
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG
1351 AAGACCCTCG TCGAGCTGGC AAGATGCTGA TGACACTGCC ACTCCTGAGG
1401 CAGACCTCTA CCAAGGCCGT GCAGCATTTC TACAACATCA AACTAGAAGG
1451 CAAAGTCCCA ATGCACAAAC TTTTTTTGGA AATGTTGGAG GCCAAGGTCT
1501 GACTAAAAGC TCCCTGGGCC TTCCCATCCT TCATGTTGAA AAAGGGAAAA
1551 TAAACCCAAG AGTGATGTCG AAGAACTTA GAGTTTAGTT AACAACATCA
1601 AAAATCAACA GACTGCACTG ATAATTTAGC AGCAAGACTA TGAAGCAGCT
1651 TTCAGATTCC TCCATAGGTT CCTGATGAGT TCTTTCTACT TTCTCCATCA
1701 TCTTCTTTCC TCTTTCTTCC CACATTTCTC TTTCTCTTA TTTTTCTCC
1751 TTTTCTTCTT TCACCTCCCT TATTTCTTTG CTTCTTTCAT TCCTAGTTCC
1801 CATTCTCCTT TATTTTCTTC CCGTCTGCCT GCCTTCTTTC TTTTCTTTAC
1851 CTACTCTCAT TCCTCTCTTT TCTCATCCTT CCCCTTTTTT CTAAATTGA
1901 AATAGCTTTA GTTTAAAAA AAAAATCCTC CCTTCCCCCT TTCCTTTCCC
1951 TTTCTTTCCCT TTTTCCCTTT CCTTTTCCCT TTCCTTTCCCT TTCCTCTTGA
2001 CCTTCTTTCC ATCTTTCTTT TTCTTCCTTC TGCTGCTGAA CTTTTAAAAG
2051 AGGTCTCTAA CTGAAGAGAG ATGGAAGCCA GCCCTGCCAA AGGATGGAGA
2101 TCCATAATAT GGATGCCAGT GAACTTATTG TGAACCATAC CGTCCCCAAT
2151 GACTAAGGAA TCAAAGAGAG AGAACCAACG TTCCTAAAAG TACAGTGCAA
2201 CATATACAAA TTGACTGAGT GCAGTATTAG ATTCATGGG AGCAGCCTCT

FIGURE 4B

2251 AATTAGACAA CTTAAGCAAC GTTGCATCGG CTGCTTCTTA TCATTGCTTT
2301 TCCATCTAGA TCAGTTACAG CCATTTGATT CCTTAATTGT TTTTCAAGT
2351 CTTCCAGGTA TTTGTTAGTT TAGCTACTAT GTAACTTTTT CAGGGAATAG
2401 TTTAAGCTTT ATTCATTCAT GCAATACTAA AGAGAAATAA GAATACTGCA
2451 ATTTTGTGCT GGCTTTGAAC AATTACGAAC AATAATGAAG GACAAATGAA
2501 TCCTGAAGGA AGATTTTAA AAATGTTTTG TTTCTTCTTA CAAATGGAGA
2551 TTTTTTTGTA CCAGCTTTAC CACTTTTCAG CCATTTATTA ATATGGGAAT
2601 TTAACCTACT CAAGCAATAG TTGAAGGGAA GGTGCATATT ATCACGGATG
2651 CAATTTATGT TGTGTGCCAG TCTGGTCCCA AACATCAATT TCTTAACATG
2701 AGCTCCAGTT TACCTAAATG TTCACTGACA CAAAGGATGA GATTACACCT
2751 ACAGTGACTC TGAGTAGTCA CATATATAAG CACTGCACAT GAGATATAGA
2801 TCCGTAGAAT TGTCAGGAGT GCACCTCTCT ACTTGGGAGG TACAATTGCC
2851 ATATGATTTC TAGCTGCCAT GGTGGTTAGG AATGTGATAC TGCCTGTTTG
2901 CAAAGTCACA GACCTTGCCT CAGAAGGAGC TGTGAGCCAG TATTCATTTA
2951 AGAGAATTCC ACCACACTGG CGGCCCGCGC TTGAT (SEQ ID NO:3)

FIGURE 4C

1 GCGGGCCGCCAGTGTGGTGGGAATTCGGCTTGTCACTAGGAGAACATTGTGTTAATTGCA 60
 -----+-----+-----+-----+-----+-----+-----+
 CGCCCGGCGGTACACCACCTTAAGCCGAACAGTGATCCTCTTGTAACACAATTAACGT

 61 CTGTGCTCTGTCAAGGAACTTTGATTTATAGCTGGGGTGCACAAATAATGGTTGCCGGT 120
 -----+-----+-----+-----+-----+-----+-----+
 GACACGAGACAGTTCCCTTTGAAACTAAATATCGACCCACGTGTTTATTACCAACGGCCA

 121 CGCACATGGATTTCGGTAGAACTTTGCCTTCCTGAATCTTTTTCCCTGCACTACGAGGAAG 180
 -----+-----+-----+-----+-----+-----+-----+
 GCGTGTAACCTAAGCCATCTTGAAACGGAAGGACTTAGAAAAAGGGACGTGATGCTCCTTC
 M D S V E L C L P E S F S L H Y E E E

 181 AGCTTCTCTGCAGAATGTCAAACAAAGATCGACACATTGATTCCAGCTGTTTCGTCTTCA 240
 -----+-----+-----+-----+-----+-----+-----+
 TCGAAGAGACGTCTTACAGTTTGTCTTAGCTGTGTAAGGTGACAAGCAGGAAGT
 L L C R M S N K D R H I D S S C S S F I

 241 TCAAGACGGAACCTTCCAGCCCAGCCTCCCTGACGGACAGCGTCAACCACCACAGCCCTG 300
 -----+-----+-----+-----+-----+-----+-----+
 AGTTCTGCCTTGGAAGGTGCGGTGCGAGGGACTGCCTGTGCGAGTTGGTGGTGTGCGGGAC
 K T E P S S P A S L T D S V N H H S P G

 301 GTGGCTCTTCAGACGCCAGTGGGAGCTACAGTTCAACCATGAATGGCCATCAGAACGGAC 360
 -----+-----+-----+-----+-----+-----+-----+
 CACCGAGAAGTCTGCGGTACCCCTCGATGTCAAGTTGGTACTTACCGGTAGTCTTGCCTG
 G S S D A S G S Y S S T M N G H Q N G L

 361 TTGACTCGCCACCTCTCTACCCTTCTGCTCCTATCCTGGGAGGTAGTGGGCCTGTCAGGA 420
 -----+-----+-----+-----+-----+-----+-----+
 AACTGAGCGGTGGAGAGATGGGAAGACGAGGATAGGACCCTCCATCACCCGGACAGTCCT
 D S P P L Y P S A P I L G G S G P V R K

 421 AACTGTATGATGACTGCTCCAGCACCATTGTTGAAGATCCCCAGACCAAGTGTGAATACA 480
 -----+-----+-----+-----+-----+-----+-----+
 TTGACATACTACTGACGAGGTGCTGGTAACAATTCTAGGGGTCTGGTTCACACTTATGT
 L Y D D C S S T I V E D P Q T K C E Y M

 481 TGCTCAACTCGATGCCCCAAGAGACTGTGTTTAGTGTGTGGTGACATCGCTTCTGGGTACC 540
 -----+-----+-----+-----+-----+-----+-----+
 ACGAGTTGAGCTACGGGTCTCTGACACAAATCACACACCACTGTAGCGAAGACCCATGG
 L N S M P K R L C L V C G D I A S G Y H

FIGURE 5A

ACTATGGGGTAGCATCATGTGAAGCCTGCAAGGCATTCTTCAAGAGGACAATTCAAGGCA
 541 -----+-----+-----+-----+-----+-----+ 600
 TGATACCCCATCGTAGTACACTTCGGACGTTCCGTAAGAAGTTCTCCTGTAAAGTTCCGT
Y G V A S C E A C K A F F K R T I Q G N
 ATATAGAATACAGCTGCCCTGCCACGAATGAATGTGAAATCACAAAGCGCAGACGTAAAT
 601 -----+-----+-----+-----+-----+-----+ 660
 TATATCTTATGTCGACGGGACGGTGCTTACTTACACTTTAGTGTTTCGCGTCTGCATTTA
I E Y S C P A T N E C E I T K R R R K S
 CCTGCCAGGCTTGCCGCTTCATGAAGTGTTTAAAGTGGGCATGCTGAAAGAAGGGGTGC
 661 -----+-----+-----+-----+-----+-----+ 720
 GGACGGTCCGAACGGCGAAGTACTTCACAAATTTTCAACCGTACGACTTTCTTCCCCACG
C Q A C R F M K C L K V G M L K E G V R
 GTCTTGACAGAGTACGTGGAGGTCGGCAGAAGTACAAGCGCAGGATAGATGCGGAGAACA
 721 -----+-----+-----+-----+-----+-----+ 780
 CAGAACTGTCTCATGCACCTCCAGCCGTCTTCATGTTTCGCGTCCTATCTACGCCTCTTGT
 L D R V R G G R Q K Y K R R I D A E N S
 GCCCATACCTGAACCCCTCAGCTGGTTCAGCCAGCCAAAAAGCCATATAACAAGATTGTCT
 781 -----+-----+-----+-----+-----+-----+ 840
 CGGGTATGGACTTGGGAGTCGACCAAGTCGGTTCGGTTTTTCGGTATATTGTTCTAACAGA
 P Y L N P Q L V Q P A K K P Y N K I V S
 CACATTTGTTGGTGGCTGAACCGGAGAAGATCTATGCCATGCCTGACCCCTACTGTCCCCG
 841 -----+-----+-----+-----+-----+-----+ 900
 GTGTAAACAACCACCGACTTGGCCTCTTCTAGATACGGTACGGACTGGGATGACAGGGGC
 H L L V A E P E K I Y A M P D P T V P D
 ACAGTGACATCAAAGCCCTCACTACACTGTGTGACTTGGCCGACCGAGAGTTGGTGGTTA
 901 -----+-----+-----+-----+-----+-----+ 960
 TGTCAGTGTAGTTTCGGGAGTGATGTGACACACTGAACCGGCTGGCTCTCAACCACCAAT
 S D I K A L T T L C D L A D R E L V V I
 TCATTGGATGGGCGAAGCATATTCCAGGCTTCTCCACGCTGTCCCTGGCGGACCAGATGA
 961 -----+-----+-----+-----+-----+-----+ 1020
 AGTAACCTACCCGCTTCGTATAAGGTCCGAAGAGGTGCGACAGGGACCGCCTGGTCTACT
 I G W A K H I P G F S T L S L A D Q M S
 GCCTTCTGCAGAGTGCTTGGATGGAAATTTTGATCCTTGGTGTCGTATACCGGTCTCTTT
 1021 -----+-----+-----+-----+-----+-----+ 1080
 CGGAAGACGTCTCACGAACCTACCTTTAAACTAGGAACACAGCATATGGCCAGAGAAA
 L L Q S A W M E I L I L G V V Y R S L S

FIGURE 5B

1081 CATTGAGGATGAACTTGTCTATGCAGACGATTATATAATGGACGAAGACCAGTCCAAAT 1140
 -----+-----+-----+-----+-----+-----+
 GTAAACTCCTACTTGAACAGATACGTCTGCTAATATATTACCTGCTTCTGGTCAGGTTTA
 F E D E L V Y A D D Y I M D E D Q S K L

 1141 TAGCAGGCCTTCTTGATCTAAATAATGCTATCCTGCAGCTGGTAAAGAAATACAAGAGCA 1200
 -----+-----+-----+-----+-----+-----+
 ATCGTCCGGAAGAACTAGATTTATTACGATAGGACGTCGACCATTCTTTATGTTCTCGT
 A G L L D L N N A I L Q L V K K Y K S M

 1201 TGAAGCTGGAAAAAGAAGAATTTGTCACCCTCAAAGCTATAGCTCTTGCTAATTCAGACT 1260
 -----+-----+-----+-----+-----+-----+
 ACTTCGACCTTTTTCTTCTTAAACAGTGGGAGTTTCGATATCGAGAACGATTAAGTCTGA
 K L E K E E F V T L K A I A L A N S D S

 1261 CCATGCACATAGAAGATGTTGAAGCCGTTTCAAGCTTCAGGATGTCTTACATGAAGCGC 1320
 -----+-----+-----+-----+-----+-----+
 GGTACGTGTATCTTCTACAACCTTCGGCAAGTCTTCGAAGTCTTACAGAATGTACTTCGCG
 M H I E D V E A V Q K L Q D V L H E A L

 1321 TGCAGGATTATGAAGCTGGCCAGCACATGGAAGACCCTCGTCGAGCTGGCAAGATGCTGA 1380
 -----+-----+-----+-----+-----+-----+
 ACGTCCTAATACTTCGACCGGTCGTGTACCTTCTGGGAGCAGCTCGACCGTTCTACGACT
 Q D Y E A G Q H M E D P R R A G K M L M

 1381 TGACACTGCCACTCCTGAGGCAGACCTCTACCAAGGCCGTGCAGCATTTCTACAACATCA 1440
 -----+-----+-----+-----+-----+-----+
 ACTGTGACGGTGAGGACTCCGTCTGGAGATGGTTCCGGCACGTCGTAAAGATGTTGTAGT
 T L P L L R Q T S T K A V Q H F Y N I K

 1441 AACTAGAAGGCAAAGTCCCAATGCACAACTTTTTTTGGAAATGTTGGAGGCCAAGGTCT 1500
 -----+-----+-----+-----+-----+-----+
 TTGATCTTCCGTTTCAGGGTTACGTGTTTGAAAAAACCTTTACAACCTCCGGTTCCAGA
 L E G K V P M H K L F L E M L E A K V *
 (SEQ ID NO:4)
 1501 GACTAAAAGCTCCCTGGGCCTTCCCATCCTTCATGTTGAAAAAGGGAAAATAAACCCAAG 1560
 -----+-----+-----+-----+-----+-----+
 CTGATTTTCGAGGGACCCGGAAGGGTAGGAAGTACAACCTTTTTCCCTTTTATTTGGGTTC

 1561 AGTGATGTCGAAGAACTTAGAGTTTAGTTAACAACATCAAAAATCAACAGACTGCACTG 1620
 -----+-----+-----+-----+-----+-----+
 TCACTACAGCTTCTTTGAATCTCAAATCAATTGTTGTAGTTTTTAGTTGTCTGACGTGAC

 1621 ATAATTTAGCAGCAAGACTATGAAGCAGCTTTCAGATTCCTCCATAGGTTTCCTGATGAGT 1680
 -----+-----+-----+-----+-----+-----+
 TATTAAATCGTCGTTCTGATACTTCGTCGAAAGTCTAAGGAGGTATCCAAGGACTACTCA

FIGURE 5C

1681 TCTTTCTACTTTCTCCATCATCTTCTTTCTCTTTCTTCCCACATTTCTCTTTCTCTTTA
-----+-----+-----+-----+-----+-----+ 1740
AGAAAGATGAAAGAGGTAGTAGAAGAAAGGAGAAAGAAGGGTGTAAAGAGAAAGAGAAAT

1741 TTTTTTCTCCTTTTCTTCTTTTACCTCCCTTATTTCTTTGCTTCTTTCATTCTCTAGTTCC
-----+-----+-----+-----+-----+-----+ 1800
AAAAAAGAGGAAAAGAAGAAAGTGGAGGGAATAAAGAAACGAAGAAAGTAAGGATCAAGG

1801 CATTCTCCTTTATTTTCTTCCCGTCTGCCTGCCTTCTTTCTTTTCTTTACCTACTCTCAT
-----+-----+-----+-----+-----+-----+ 1860
GTAAGAGGAAATAAAAGAAGGGCAGACGGACGGAAGAAAGAAAAGAAATGGATGAGAGTA

1861 TCCTCTCTTTTCTCATCCTTCCCCTTTTTTCTAAATTTGAAATAGCTTTAGTTTAAAAAA
-----+-----+-----+-----+-----+-----+ 1920
AGGAGAGAAAAGAGTAGGAAGGGGAAAAAGATTTAACTTTATCGAAATCAAATTTTTT

1921 AAAATCCTCCCTTCCCCCTTTCCTTTCCCTTTCTTTCCTTTTCCCTTTCCTTTTCCCT
-----+-----+-----+-----+-----+-----+ 1980
TTTTTAGGAGGGAAGGGGAAAGGAAAGGAAAGAAAGGAAAAGGGAAGGAAAAGGGA

1981 TTCCTTTCCCTTTCCTCTTGACCTTCTTCCATCTTCTTTTCTTCCCTTCTGCTGCTGAA
-----+-----+-----+-----+-----+-----+ 2040
AAGGAAAGGAAAGGAGAACTGGAAGAAAGGTAGAAAGAAAAGAAGGAAGACGACGACTT

2041 CTTTTAAAGAGGTCTCTAACTGAAGAGAGATGGAAGCCAGCCCTGCCAAAGGATGGAGA
-----+-----+-----+-----+-----+-----+ 2100
GAAATTTTCTCCAGAGATTGACTTCTCTACCTTCGGTCGGGACGGTTTCCTACCTCT

2101 TCCATAATATGGATGCCAGTGAACCTATTGTGAACCATACCGTCCCCAATGACTAAGGAA
-----+-----+-----+-----+-----+-----+ 2160
AGGTATTATACCTACGGTCACTTGAATAACACTTGGTATGGCAGGGGTACTGATTCCTT

2161 TCAAAGAGAGAGAACCAACGTTCCCTAAAAGTACAGTGCAACATATACAAATTGACTGAGT
-----+-----+-----+-----+-----+-----+ 2220
AGTTTCTCTCTCTTGGTTGCAAGGATTTTCATGTCACGTTGTATATGTTTAACTGACTCA

2221 GCAGTATTAGATTTTCATGGGAGCAGCCTCTAATTAGACAACTTAAGCAACGTTGCATCGG
-----+-----+-----+-----+-----+-----+ 2280
CGTCATAATCTAAAGTACCCTCGTCGGAGATTAATCTGTTGAATTCGTTGCAACGTAGCC

2281 CTGCTTCTTATCATTTGCTTTTCCATCTAGATCAGTTACAGCCATTTGATTCCTTAATTGT
-----+-----+-----+-----+-----+-----+ 2340
GACGAAGAATAGTAACGAAAAGGTAGATCTAGTCAATGTCGGTAAACTAAGGAATTAACA

FIGURE 5D

2341 TTTTCAAGTCTTCCAGGTATTTGTTAGTTTAGCTACTATGTAACCTTTTTCAGGGAATAG 2400
 -----+-----+-----+-----+-----+-----+
 AAAAAGTTT CAGAAGGTCCATAAACAATCAAATCGATGATACATTGAAAAAGTCCCTTATC

 2401 TTTAAGCTTTTATTCATTCATGCAATACTAAAGAGAAATAAGAATACTGCAATTTTGTGCT 2460
 -----+-----+-----+-----+-----+-----+
 AAATTCGAAATAAGTAAGTACGTTATGATTTCTCTTTATTCTTATGACGTTAAACACGA

 2461 GGCTTTGAACAATTACGAACAATAATGAAGGACAAATGAATCCTGAAGGAAGATTTTAA 2520
 -----+-----+-----+-----+-----+-----+
 CCGAAACTTGTTAATGCTTGTTATTACTTCCTGTTTACTTAGGACTTCCTTCTAAAAATT

 2521 AAATGTTTTGTTTCTTCTTACAAATGGAGATTTTTTTGTACCAGCTTTACCACTTTTCAG 2580
 -----+-----+-----+-----+-----+-----+
 TTTACAAAACAAGAAGAATGTTACCTCTAAAAAACATGGTCGAAATGGTGAAAAGTC

 2581 CCATTTATTAATATGGGAATTTAACTTACTCAAGCAATAGTTGAAGGGAAGGTGCATATT 2640
 -----+-----+-----+-----+-----+-----+
 GGTAATAAATTATACCCTTAAATTGAATGAGTTCGTTATCAACTTCCCTTCCACGTATAA

 2641 ATCACGGATGCAATTTATGTTGTGTGCCAGTCTGGTCCCAAACATCAATTTCTTAACATG 2700
 -----+-----+-----+-----+-----+-----+
 TAGTGCCTACGTTAAATACAACACACGGTCAGACCAGGGTTTGTAGTTAAAGAATTGTAC

 2701 AGCTCCAGTTTACCTAAATGTTCACTGACACAAAGGATGAGATTACACCTACAGTGACTC 2760
 -----+-----+-----+-----+-----+-----+
 TCGAGGTCAAATGGATTTACAAGTGACTGTGTTTCTACTCTAATGTGGATGTCACTGAG

 2761 TGAGTAGTCACATATATAAGCACTGCACATGAGATATAGATCCGTAGAATTGTCAGGAGT 2820
 -----+-----+-----+-----+-----+-----+
 ACTCATCAGTGTATATATTCGTGACGTGTACTCTATATCTAGGCATCTTAACAGTCCTCA

 2821 GCACCTCTCTACTTGGGAGGTACAATTGCCATATGATTTCTAGCTGCCATGGTGGTTAGG 2880
 -----+-----+-----+-----+-----+-----+
 CGTGGAGAGATGAACCCTCCATGTTAACGGTATACTAAAGATCGACGGTACCACCAATCC

 2881 AATGTGATACTGCCTGTTTGCAAAGTCACAGACCTTGCTCAGAAGGAGCTGTGAGCCAG 2940
 -----+-----+-----+-----+-----+-----+
 TTACACTATGACGGACAAACGTTTTCAGTGTCTGGAACGGAGTCTTCCTCGACACTCGGTC

 2941 TATTCATTTAAGAGAATTCCACCACACTGGCGGCCCGCGCTTGAT (SEQ ID NO:3) 2985
 -----+-----+-----+-----+-----+
 ATAAGTAAATTCTCTTAAGGTGGTGTGACCGCCGGGCGCGAACTA (SEQ ID NO:30)

FIGURE 5E

1 MDSVELCLPE SFSLHYEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT
51 DSVNHHSPGG SSDASGSYSS TMNGHQGLD SPPLYPSAPI LGGSGPVRKL
101 YDDCSSTIVE DPQTKCEYML NSMPKRLCLV CGDIASGYHY GVASCEACKA
151 FFKRTIQGNI EYSCPATNEC EITKRRRKSC QACRFMKCLK VGMLKEGVRL
201 DRVRGGRQKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TSLADQMSL
301 LQSAWMEILI LGVVYRSLSF EDELVEADDY IMDEDQSKLA GLLDLNNAIL
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ
401 DYEAGQHMED PRRAGKMLMT LPLLROTSTK AVQHFYNIKL EGKVPMHKLF
451 LEMLEAKV* (SEQ ID NO:4)

FIGURE 6

1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA GAACATTTGT
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTTAT AGCTGGGGTG
101 CACAAATAAT GGTTGCCGGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CCTTCTGCTC CTATCCTGGG
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGA CTGCTCC AGCACCATTG
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCCAAG
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAAGTGGG
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTGCGCAGA
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG
901 ACAGTGACAT CAAAGCCCTC ACTACACTGT GTGACTTGGC CGACCGAGAG
951 TTGGTGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAAATTT

FIGURE 7A

1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGAACCTGTC
1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAGAAA TACAAGAGCA
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTT AGAAGCTTCA
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG
1351 AGAAGACCCT CGTCGAGCTG GCAAGATGCT GATGACACTG CCACTCCTGA
1401 GGCAGACCTC TACCAAGGCC GTGCAGCATT TCTACAACAT CAACTAGAA
1451 GGCAAAGTCC CAATGCACAA ACTTTTTTTT GAAATGTTGG AGGCCAAGGT
1501 CTGACTAAAA GCTCCCTGGG CCTTCCCATC CTTTCATGTTG AAAAAGGGAA
1551 AATAAACCCA AGAGTGATGT CGAAGAACT TAGAGTTTAG TTAACAACAT
1601 CAAAAATCAA CAGACTGCAC TGATAATTTA GCAGCAAGAC TATGAAGCAG
1651 CTTTCAGATT CCTCCATAGG TTCCTGATGA GTTCTTTCTA CTTTCTCCAT
1701 CATCTTCTTT CCTCTTTCTT CCCACATTC TCTTTCTCTT TATTTTTTCT
1751 CCTTTCTTC TTTCACCTCC CTTATTTCTT TGCTTCTTTC ATTCCTAGTT
1801 CCCATTCTCC TTTATTTTCT TCCCGTCTGC CTGCCTTCTT TCTTTTCTTT
1851 ACCTACTCTC ATTCCTCTCT TTTCTCATCC TTCCCCTTTT TTCTAAATTT
1901 GAAATAGCTT TAGTTTAAAA AAAAAATCC TCCCTTCCCC CTTTCCTTTC
1951 CCTTTCTTTC CTTTTTCCCT TTCCTTTTCC CTTTCCTTTC CTTTCCTCTT
2001 GACCTTCTTT CCATCTTTCT TTTTCTTCCT TCTGCTGCTG AACTTTTAAA
2051 AGAGGTCTCT AACTGAAGAG AGATGGAAGC CAGCCCTGCC AAAGGATGGA

FIGURE 7B

2101 GATCCATAAT ATGGATGCCA GTGAACTTAT TGTGAACCAT ACCGTCCCCA
2151 ATGACTAAGG AATCAAAGAG AGAGAACCAA CGTTCCTAAA AGTACAGTGC
2201 AACATATACA AATTGACTGA GTGCAGTATT AGATTTCATG GGAGCAGCCT
2251 CTAATTAGAC AACTTAAGCA ACGTTGCATC GGCTGCTTCT TATCATTGCT
2301 TTTCCATCTA GATCAGTTAC AGCCATTGA TTCCTTAATT GTTTTTTCAA
2351 GTCTTCCAGG TATTTGTTAG TTTAGCTACT ATGTAACTTT TTCAGGGAAT
2401 AGTTTAAGCT TTATTCATTC ATGCAATACT AAAGAGAAAT AAGAATACTG
2451 CAATTTTGTG CTGGCTTTGA ACAATTACGA ACAATAATGA AGGACAAATG
2501 AATCCTGAAG GAAGATTTTT AAAAATGTTT TGTTTCTTCT TACAAATGGA
2551 GATTTTTTTG TACCAGCTTT ACCACTTTTC AGCCATTTAT TAATATGGGA
2601 ATTTAACTTA CTCAAGCAAT AGTTGAAGGG AAGGTGCATA TTATCACGGA
2651 TGCAATTTAT GTTGTGTGCC AGTCTGGTCC CAAACATCAA TTTCTTAACA
2701 TGAGCTCCAG TTTACCTAAA TGTTCACTGA CACAAAGGAT GAGATTACAC
2751 CTACAGTGAC TCTGAGTAGT CACATATATA AGCACTGCAC ATGAGATATA
2801 GATCCGTAGA ATTGTCAGGA GTGCACCTCT CTA CTGTTGGA GGTACAATTG
2851 CCATATGATT TCTAGCTGCC ATGGTGGTTA GGAATGTGAT ACTGCCTGTT
2901 TGCAAAGTCA CAGACCTTGC CTCAGAAGGA GCTGTGAGCC AGTATTCATT
2951 TAAGAGAATT CCACCACACT GGCGGCCCGC GCTTGAT (SEQ ID NO:5)

FIGURE 7C

19999Y

1 MDSVELCLPE SFSLHYEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT
51 DSVNHHSPGG SSDASGSYSS TMNGHQGLD SPPLYPSAPI LGGSGPVRKL
101 YDDCSSTIVE DPQTKCEYML NSMPKRLCLV CGDIASGYHY GVASCEACKA
151 FFKRTIQGNI EYSCPATNEC EITKRRRKSC QACRFMKCLK VGMLKEGVRL
201 DRVRRGGRQKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TISLADQMSL
301 LQSAWMEILI LGVVYRSLSF EDELVIADDY IMDEDQSKLA GLLDLNNAIL
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ
401 DYEAGQHMEK TLVELARC* (SEQ ID NO:6)

FIGURE 8

20250404 10:44:50